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Sequence Listing could not be accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=27; hr=8; min=47; sec=31; ms=793;]

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Reviewer Comments:

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<211> 1310

<212> PRT

<213> Varicella zoster

<220>

<221> misc_feature

<222> (99)..(99)

<223> The 'Xaa' at location 99 stands for Thr, or Met.

<220>

<221> misc_feature

<222> (512)..(512)

<223> The 'Xaa' at location 512 stands for Ala, or Val.

<220>

<221> misc_feature

<222> (1275)..(1275)

<223> The 'Xaa' at location 1275 stands for Ser, Leu, or Xaa.

The above <223> response describing "Xaa" at location 1275 contains an
error: "Xaa" can only represent an actual amino acid; "Xaa" cannot
represent an Xaa.

Application No: 10591787 Version No: 1.0

Input Set:

Output Set:

Started: 2009-05-19 13:25:27.500
Finished: 2009-05-19 13:25:45.311
Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 811 ms
Total Warnings: 5
Total Errors: 0
No. of SeqIDs Defined: 91
Actual SeqID Count: 91

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)

SEQUENCE LISTING

<110> Nagaike, Kazuhiro
Mori, Yasuko
Gomi, Yasuyuki
Takahashi, Michiaki
Kouichi, Yamanishi

<120> Recombinant varicella-zoster virus

<130> 59150-8037

<140> 10591787

<141> 2009-05-19

<150> PCT/JP2005/003652

<151> 2005-03-05

<150> JP 2004-063277

<151> 2004-03-05

<160> 91

<170> PatentIn version 3.2

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Met Asp Thr
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Leu Glu Leu Met Asp Leu Leu Asp Ala Ala Ala Ala Ala Glu His
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Arg Ala Arg Val Val Thr Ser Ser Gln Pro Asp Asp Leu Leu Phe Gly
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Glu Asn Gly Val Met Val Gly Arg Glu His Glu Ile Val Ser Ile Pro
55 60 65
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Ser Val Ser Gly Leu Gln Pro Glu Pro Arg Thr Glu Asp Val Gly Glu
70 75 80

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85 90 95	
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Gly Ser Pro Val Ile Pro Leu Ala Glu Val Phe His Thr Arg Phe Ser	
100 105 110 115	
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Glu Ala Gly Ala Arg Glu Pro Thr Gly Ala Asp Arg Ser Leu Glu Thr	
120 125 130	
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Val Ser Leu Gly Thr Lys Leu Ala Arg Ser Pro Lys Pro Pro Met Asn	
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Asp Gly Glu Thr Gly Arg Gly Thr Thr Pro Pro Phe Pro Gln Ala Phe	
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Ser Pro Val Ser Pro Ala Ser Pro Val Gly Asp Ala Ala Gly Asn Asp	
165 170 175	
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Gln Arg Glu Asp Gln Arg Ser Ile Pro Arg Gln Thr Thr Arg Gly Asn	
180 185 190 195	
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Ser Pro Gly Leu Pro Ser Val Val His Arg Asp Arg Gln Thr Gln Ser	
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Ile Ser Gly Lys Lys Pro Gly Asp Glu Gln Ala Gly His Ala His Ala	
215 220 225	
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Ser Gly Asp Gly Val Val Leu Gln Lys Thr Gln Arg Pro Ala Gln Gly	
230 235 240	
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Lys Ser Pro Lys Lys Lys Thr Leu Lys Val Lys Val Pro Leu Pro Ala	
245 250 255	
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Arg Lys Pro Gly Gly Pro Val Pro Gly Pro Val Glu Gln Leu Tyr His	
260 265 270 275	
gtc ctt tcg gac agc gtt ccc gct aag ggg gca aag gcg gac ctg ccg	1101
Val Leu Ser Asp Ser Val Pro Ala Lys Gly Ala Lys Ala Asp Leu Pro	
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Phe Glu Thr Asp Asp Thr Arg Pro Arg Lys His Asp Ala Arg Gly Ile	
295 300 305	

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Thr Pro Arg Val Pro Gly Arg Ser Ser Gly Gly Lys Pro Arg Ala Phe	
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Leu Ala Leu Pro Gly Arg Ser His Ala Pro Asp Pro Ile Glu Asp Asp	
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Ser Ser Ser Ser Ser Trp Gly Ser Ser Ser Glu Asp Glu Asp Asp Glu	
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Pro Arg Arg Val Ser Val Gly Ser Glu Thr Thr Gly Ser Arg Ser Gly	
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Arg Glu His Ala Pro Ser Pro Ser Asn Ser Asp Asp Ser Asp Ser Asn	
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gat ggt ggg tcg acg aaa caa aat atc caa ccg gga tat cga tcc atc	1485
Asp Gly Gly Ser Thr Lys Gln Asn Ile Gln Pro Gly Tyr Arg Ser Ile	
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Ser Gly Pro Asp Pro Arg Ile Arg Lys Thr Lys Arg Leu Ala Gly Glu	
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Pro Gly Arg Gln Arg Gln Lys Ser Phe Ser Leu Pro Arg Ser Arg Thr	
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Pro Ile Ile Pro Pro Val Ser Gly Pro Leu Met Met Pro Asp Gly Ser	
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Pro Trp Pro Gly Ser Ala Pro Leu Pro Ser Asn Arg Val Arg Phe Gly	
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Pro Ser Gly Glu Thr Arg Glu Gly His Trp Glu Asp Glu Ala Val Arg	
485 490 495	
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Ala Ala Arg Ala Arg Tyr Glu Ala Ser Thr Glu Pro Xaa Pro Leu Tyr	
500 505 510 515	
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Val Pro Glu Leu Gly Asp Pro Ala Arg Gln Tyr Arg Ala Leu Ile Asn	
520 525 530	
ctg atc tac tgt cca gac aga gac cct ata gca tgg ctc cag aac ccc	1869

Leu Ile Tyr Cys Pro Asp Arg Asp Pro Ile Ala Trp Leu Gln Asn Pro	
535 540 545	
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Lys Leu Thr Gly Val Asn Ser Ala Leu Asn Gln Phe Tyr Gln Lys Leu	
550 555 560	
ttg cca ccg gga cgg gcg ggt acc gcc gtt acg ggg agc gta gcg tct	1965
Leu Pro Pro Gly Arg Ala Gly Thr Ala Val Thr Gly Ser Val Ala Ser	
565 570 575	
ccc gtt ccg cat gta ggc gaa gcc atg gcc acg ggg gag gcc ctc tgg	2013
Pro Val Pro His Val Gly Glu Ala Met Ala Thr Gly Glu Ala Leu Trp	
580 585 590 595	
gct ctc ccc cac gcg gcc gcg gcc gtg gct atg agc cgt cgg tac gac	2061
Ala Leu Pro His Ala Ala Ala Val Ala Met Ser Arg Arg Tyr Asp	
600 605 610	
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Arg Ala Gln Lys His Phe Ile Leu Gln Ser Leu Arg Arg Ala Phe Ala	
615 620 625	
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Ser Arg Gly His Pro Ser Pro Thr Thr Pro Ala Thr Gln Thr Pro Asp	
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Asp Arg Leu Arg Thr Pro Arg Lys Arg Lys Ser Gln Pro Val Glu Ser	
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Arg Ser Leu Leu Asp Lys Ile Arg Glu Thr Pro Val Ala Asp Ala Arg	
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Val Ala Asp Asp His Val Val Ser Lys Ala Lys Arg Arg Val Ser Glu	
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Pro Val Thr Ile Thr Ser Gly Pro Val Val Asp Pro Pro Ala Val Ile	
725 730 735	
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Thr Met Pro Leu Asp Gly Pro Ala Pro Asn Gly Gly Phe Arg Arg Ile	
740 745 750 755	
ccc cgg ggg gcc ctg cat acc ccg gtc ccg tcg gac cag gct cgc aag	2541
Pro Arg Gly Ala Leu His Thr Pro Val Pro Ser Asp Gln Ala Arg Lys	

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Ala Tyr Cys Thr Pro Glu Thr Ile Ala Arg Leu Val Asp Asp Pro Leu			
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Phe Pro Thr Ala Trp Arg Pro Ala Leu Ser Phe Asp Pro Gly Ala Leu			
790	795	800	
gcg gaa atc gcc gct cgg cgt ccg ggc gga gga gac cga cgg ttt ggt			2685
Ala Glu Ile Ala Ala Arg Arg Pro Gly Gly Gly Asp Arg Arg Phe Gly			
805	810	815	
cca ccc agc gga gtg gag gcg ctg cga cgg agg tgc gcc tgg atg cgg			2733
Pro Pro Ser Gly Val Glu Ala Leu Arg Arg Arg Cys Ala Trp Met Arg			
820	825	830	835
cag atc cca gac ccg gag gat gtg agg ctt ctg atc atc tac gat ccg			2781
Gln Ile Pro Asp Pro Glu Asp Val Arg Leu Leu Ile Ile Tyr Asp Pro			
840	845	850	
ttg ccc gga gag gac atc aac ggc ccc ctc gag agc acc ctc gcg aca			2829
Leu Pro Gly Glu Asp Ile Asn Gly Pro Leu Glu Ser Thr Leu Ala Thr			
855	860	865	
gat ccg gga ccg tca tgg agt cca tcc cga ggg gga ctg tct gtg gtc			2877
Asp Pro Gly Pro Ser Trp Ser Pro Ser Arg Gly Gly Leu Ser Val Val			
870	875	880	
ctg gca gcc ctg agt aac cgg ttg tgc ctg ccg agc act cat gcc tgg			2925
Leu Ala Ala Leu Ser Asn Arg Leu Cys Leu Pro Ser Thr His Ala Trp			
885	890	895	
gcc ggg aac tgg acc ggc ccg ccg gac gtg tcc gct ttg aac gcc cgg			2973
Ala Gly Asn Trp Thr Gly Pro Pro Asp Val Ser Ala Leu Asn Ala Arg			
900	905	910	915
ggc gtt tta tta ctg tcg acc cga gac ctg gcc ttt gcc ggg gcc gtc			3021
Gly Val Leu Leu Leu Ser Thr Arg Asp Leu Ala Phe Ala Gly Ala Val			
920	925	930	
gag tat cta ggc tcg cgg ttg gcc tct gcc cgg cgc cgg ttg ctg gtg			3069
Glu Tyr Leu Gly Ser Arg Leu Ala Ser Ala Arg Arg Arg Leu Leu Val			
935	940	945	
ttg gac gcg gtg gcc ctc gag agg tgg ccc ggg gat gga ccc gct ttg			3117
Leu Asp Ala Val Ala Leu Glu Arg Trp Pro Gly Asp Gly Pro Ala Leu			
950	955	960	
tct cag tat cac gtg tac gtc cgg gcc ccg gcg cga ccg gac gcc cag			3165
Ser Gln Tyr His Val Tyr Val Arg Ala Pro Ala Arg Pro Asp Ala Gln			
965	970	975	
gcc gtc gtc cga tgg cca gac tcg gcg gtc aca gaa gga ctc gcc cgg			3213
Ala Val Val Arg Trp Pro Asp Ser Ala Val Thr Glu Gly Leu Ala Arg			
980	985	990	995

gcc gtg ttt gca tgc	tgc cgc acc ttt ggg	cca gcg agt ttt gct	3258
Ala Val Phe Ala Ser	Ser Arg Thr Phe Gly	Pro Ala Ser Phe Ala	
1000	1005	1010	
cg t atc gag act gcg	ttt gcc aac ctg tac	ccg ggc gaa caa ccc	3303
Arg Ile Glu Thr Ala	Phe Ala Asn Leu Tyr	Pro Gly Glu Gln Pro	
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ctg tgt ttg tgc cgc	ggg ggc aac gtc gca	tac acc gtg tgt acc	3348
Leu Cys Leu Cys Arg	Gly Gly Asn Val Ala	Tyr Thr Val Cys Thr	
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cgc gcg ggc ccc aag	acc cgc gtc ccc ctg	tgc ccc cgt gaa tac	3393
Arg Ala Gly Pro Lys	Thr Arg Val Pro Leu	Ser Pro Arg Glu Tyr	
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Arg Gln Tyr Val Leu	Pro Gly Phe Asp Gly	Cys Lys Asp Leu Ala	
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Arg Gln Ser Arg Gly	Leu Gly Leu Gly Ala	Ala Asp Phe Val Asp	
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Ala Ala Gly Pro Glu	Ala Gly Asp Val Pro	Thr Trp Ala Arg Val	
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Ser Ala Asp Glu Ala	Arg Asn Ala Leu Pro	Pro Ile Pro Arg Val	
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Arg Pro Ala Glu Thr	Gln Ala Gly Arg Gln	Arg Arg Thr Ala Asp	
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Asp Arg Glu His Ala	Leu Glu Pro Asp Asp	Trp Glu Val Gly Cys	
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Gly Val Leu Arg Asp	Arg Arg Val Gly Xaa	Arg Pro Ala Val Lys	
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